

Amendments to the Claims

This listing of claims replaces all prior versions and listings of claims in the application.

Listing of Claims:

1. (Currently amended) A program which allows a computer to execute the processes of:
producing a control virtual two-dimensional electrophoresis pattern [[deduced by analyzing]], wherein the production comprises analyzing genomic nucleotide sequence information, comparing said control two-dimensional electrophoresis pattern and a target two-dimensional electrophoresis pattern obtained by performing two-dimensional electrophoresis using target genomic DNA, and
detecting a difference in spot position between said control two-dimensional electrophoresis pattern and said target two-dimensional electrophoresis pattern.
2. (Previously presented) The program according to claim 1, wherein, in said process of producing the control two-dimensional electrophoresis pattern, the control two-dimensional electrophoresis pattern is produced by detecting the recognition sequence of a first restriction enzyme and the recognition sequence of a second restriction enzyme in said genomic nucleotide sequence information, wherein the genomic sequence information comprises a nucleotide sequence flanked by the first restriction enzyme recognition sequence and the second restriction enzyme recognition sequence and another nucleotide sequence flanked by the two first restriction enzyme recognition sequences.
3. (Original) The program according to claim 2, wherein said first restriction enzyme and said second restriction enzyme are selected from methylation insensitive restriction enzymes.

4. (Original) The program according to claim 2, wherein said first restriction enzyme and said second restriction enzyme are selected from methylation sensitive restriction enzymes.
5. (Previously presented) The program according to claim 1, which comprises a process of obtaining said genomic nucleotide sequence information from a genetic sequence database by means of a communication line network.
6. (Original) The program according to claim 1, wherein, in said process of producing the control two-dimensional electrophoresis pattern, a plurality of spots are produced based on genomic nucleotide sequence information and these spots are linked to gene loci information on a genome.
7. (Original) The program according to claim 1, wherein, in said process of producing the control two-dimensional electrophoresis pattern based on a genomic nucleotide sequence information, abnormal information comprised in said genomic nucleotide sequence information is detected.
8. (Original) The program according to claim 7, which links the detected abnormal information to a spot comprised in the produced two-dimensional electrophoresis pattern in order to memorize the information.
9. (Withdrawn) A method for analyzing genomic DNA which comprises the steps of:
 - producing a two-dimensional electrophoresis pattern by performing two-dimensional electrophoresis using a target genomic DNA,
 - comparing said two-dimensional electrophoresis pattern and a control two-dimensional electrophoresis pattern produced based on genomic nucleotide sequence information, and
 - detecting a difference in spot position between said control two-dimensional electrophoresis pattern and said target two-dimensional electrophoresis pattern.

10. (Withdrawn) The method for analyzing genomic DNA according to claim 9, which comprises a step of extracting said target genomic DNA from plant cells.

11. (Withdrawn) The method for analyzing genomic DNA according to claim 9, wherein said target genomic DNA is derived from a higher organism.

12. (Withdrawn) The method for analyzing genomic DNA according to claim 9, wherein, in said step of producing the two-dimensional electrophoresis pattern of said target genomic DNA by the following steps (a) to (e):

- (a) treating genomic DNA with a first restriction enzyme,
- (b) adding a label to a site cleaved with said restriction enzyme,
- (c) performing a first-dimension fractionation on the obtained DNA fragment by electrophoresis,
- (d) after treating the DNA fragment fractioned in step (c) with a second restriction enzyme, performing a second-dimension fractionation, and
- (e) detecting a spot of the labeled DNA fragment fractioned in step (d).

13. (Withdrawn) The method for analyzing genomic DNA according to claim 12, wherein, after said step (b), the obtained DNA fragment is treated with a restriction enzyme different from the first and second restriction enzymes and before said step (c) is performed.

14. (Withdrawn) The method for analyzing genomic DNA according to claim 12, which comprises detecting the recognition sequences of said first and second restriction enzymes in genomic nucleotide sequence information, and producing the control two electrophoresis pattern based on these cleavage sites.

15. (Withdrawn) The method for analyzing genomic DNA according to claim 12, wherein said step (b) is carried out by connecting one end of an adapter to the restriction enzyme cleavage site as well as adding said label to the other end of said adapter.

16. (Withdrawn) The method for analyzing genomic DNA according to claim 9, wherein said control two-dimensional electrophoresis pattern has a plurality of spots produced based on genomic nucleotide sequence information and links these spots to gene loci information on a genome.

17. (Withdrawn) The method for analyzing genomic DNA according to claim 9, which comprises detecting abnormal information comprised in genomic nucleotide sequence information before producing the control two-dimensional electrophoresis pattern based on said genomic nucleotide sequence information.

18. (Withdrawn) The method for analyzing genomic DNA according to claim 17, which comprises linking the detected abnormal information to a spot comprised in the produced two-dimensional electrophoresis pattern.

19. (Withdrawn) A method for identifying genes associated with mutant genes and/or mutant traits, which comprises detecting mutated sites in target genomic DNA by the method for analyzing genomic DNA according to claim 9.

20. (Withdrawn) A method for isolating genes associated with mutant genes and/or mutant traits, which comprises isolating a DNA fragment containing mutated sites detected by the identification method according to claim 19, from said two-dimensional electrophoresis pattern.

21. (Withdrawn) A two-dimensional electrophoresis pattern, which has a plurality of spots produced based on genomic nucleotide sequence information and estimated from said genomic nucleotide sequence information.

22. (Withdrawn) The two-dimensional electrophoresis pattern according to claim 21, wherein said plurality of spots are linked to gene loci information on a genome.

23. (Withdrawn) The two-dimensional electrophoresis pattern according to claim 21, wherein said genomic nucleotide sequence information is nucleotide sequence information obtained from a plant nuclear genome.

24. (Withdrawn) The two-dimensional electrophoresis pattern according to claim 21, wherein abnormal information detected from said genomic nucleotide sequence information is linked to said plurality of spots.

25. (Withdrawn) The two-dimensional electrophoresis pattern according to claim 21, wherein said genomic nucleotide sequence information is obtained from the genome of a higher organism.